

TECH CENTER 1600/2900

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/590,447

DATE: 09/14/2001

TIME: 11:03:39

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09142001\I590447.raw

ENTERED

4 <110> APPLICANT: Forman, Barry M.
5 Beard, Richard L.
6 Chandraratna, Roshantha A.
8 <120> TITLE OF INVENTION: Methods for Modulating FXR Receptor
9 Activity
11 <130> FILE REFERENCE: 17302
13 <140> CURRENT APPLICATION NUMBER: 09/590,447
14 <141> CURRENT FILING DATE: 2000-06-09
16 <150> PRIOR APPLICATION NUMBER: 60/138,986
17 <151> PRIOR FILING DATE: 1999-06-11
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 469
25 <212> TYPE: PRT
26 <213> ORGANISM: Rattus norvegicus
28 <400> SEQUENCE: 1
29 Met Asn Leu Ile Gly Pro Ser His Leu Gln Ala Thr Asp Glu Phe Ala
30 1 5 10 15
31 Leu Ser Glu Asn Leu Phe Gly Val Leu Thr Glu His Ala Ala Gly Pro
32 20 25 30
33 Leu Gly Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val
34 35 40 45
35 Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser Tyr Tyr Ser
36 50 55 60
37 Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Asp Trp Tyr Ser Pro Gly
38 65 70 75 80
39 Leu Tyr Glu Leu Arg Arg Met Pro Thr Glu Ser Val Tyr Gln Gly Glu
40 85 90 95
41 Thr Glu Val Ser Glu Met Pro Val Thr Lys Lys Pro Arg Met Ala Ala
42 100 105 110
43 Ser Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val Cys Gly
44 115 120 125
45 Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys
46 130 135 140
47 Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val Tyr Lys Cys
48 145 150 155 160
49 Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg Arg Lys Cys
50 165 170 175
51 Gln Asp Cys Arg Leu Arg Lys Cys Arg Glu Met Gly Met Leu Ala Glu
52 180 185 190
53 Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu Arg Lys Asn
54 195 200 205
55 Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser Glu Gly Arg
56 210 215 220
57 Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Leu Cys Arg Glu Lys Thr
58 225 230 235 240

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59 Glu Leu Thr Val Asp Gln Gln Thr Leu Leu Asp Tyr Ile Met Asp Ser
60      245      250      255
61 Tyr Ser Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile Leu Lys
62      260      265      270
63 Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu Met Ala
64      275      280      285
65 Thr Ser His Val Gln Ile Leu Val Glu Phe Thr Lys Arg Leu Pro Gly
66      290      295      300
67 Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys Gly Ser
68      305      310      315      320
69 Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn Lys Lys
70      325      330      335
71 Leu Pro Ala Gly His Ala Asp Leu Leu Glu Glu Arg Ile Arg Lys Ser
72      340      345      350
73 Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr Lys Ser
74      355      360      365
75 Val Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu Thr Ala
76      370      375      380
77 Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg Glu Ala
78      385      390      395      400
79 Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys Leu Cys
80      405      410      415
81 Lys Ile Tyr Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu Leu Gly
82      420      425      430
83 Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu Met Leu
84      435      440      445
85 Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu Cys Glu
86      450      455      460
87 Ile Trp Asp Val Gln
88      465
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 484
92 <212> TYPE: PRT
93 <213> ORGANISM: Mus musculus
95 <400> SEQUENCE: 2
96 Met Val Met Gln Phe Gln Gly Leu Glu Asn Pro Ile Gln Ile Ser Leu
97 1      5      10      15
98 His His Ser His Arg Leu Ser Gly Phe Val Pro Asp Gly Met Ser Val
99      20      25      30
100 Lys Pro Ala Lys Gly Met Leu Thr Glu His Ala Ala Gly Pro Leu Gly
101      35      40      45
102 Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val Pro Phe
103      50      55      60
104 Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser Tyr Tyr Ser Asn Leu
105      65      70      75      80
106 Gly Phe Tyr Pro Gln Gln Pro Glu Asp Trp Tyr Ser Pro Gly Ile Tyr
107      85      90      95
108 Glu Leu Arg Arg Met Pro Ala Glu Thr Gly Tyr Gln Gly Glu Thr Glu
109      100      105      110

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110 Val Ser Glu Met Pro Val Thr Lys Lys Pro Arg Met Ala Ala Ala Ser
111      115      120      125
112 Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val Cys Gly Asp Arg
113      130      135      140
114 Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly
115      145      150      155      160
116 Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val Tyr Lys Cys Lys Asn
117      165      170      175
118 Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg Arg Lys Cys Gln Glu
119      180      185      190
120 Cys Arg Leu Arg Lys Cys Arg Glu Met Gly Met Leu Ala Glu Cys Leu
121      195      200      205
122 Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu Arg Lys Asn Val Lys
123      210      215      220
124 Gln His Ala Asp Gln Thr Val Asn Glu Asp Asp Ser Glu Gly Arg Asp
125      225      230      235      240
126 Leu Arg Gln Val Thr Ser Thr Thr Lys Phe Cys Arg Glu Lys Thr Glu
127      245      250      255
128 Leu Thr Ala Asp Gln Gln Thr Leu Leu Asp Tyr Ile Met Asp Ser Tyr
129      260      265      270
130 Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile Leu Lys Glu
131      275      280      285
132 Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu Met Ala Thr
133      290      295      300
134 Ser His Val Gln Ile Leu Val Glu Phe Thr Lys Lys Leu Pro Gly Phe
135      305      310      315      320
136 Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys Gly Ser Ala
137      325      330      335
138 Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn Lys Lys Leu
139      340      345      350
140 Pro Ala Gly His Ala Asp Leu Leu Glu Glu Arg Ile Arg Lys Ser Gly
141      355      360      365
142 Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr Lys Ser Val
143      370      375      380
144 Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu Thr Ala Ile
145      385      390      395      400
146 Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg Glu Ala Val
147      405      410      415
148 Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys Leu Cys Lys
149      420      425      430
150 Met Tyr Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu Leu Gly Arg
151      435      440      445
152 Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu Met Leu Met
153      450      455      460
154 Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu Cys Glu Ile
155      465      470      475      480
156 Trp Asp Val Gln
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 472

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161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 3
165 Met Gly Ser Lys Met Asn Leu Ile Glu His Ser His Leu Pro Thr Thr
166   1           5           10           15
167 Asp Glu Phe Ser Phe Ser Glu Asn Leu Phe Gly Val Leu Thr Glu Gln
168           20           25           30
169 Val Ala Gly Pro Leu Gly Gln Asn Leu Glu Val Glu Pro Tyr Ser Gln
170           35           40           45
171 Tyr Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser
172           50           55           60
173 Ser Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp
174           65           70           75           80
175 Tyr Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu
176           85           90           95
177 Tyr Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro
178           100          105          110
179 Arg Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val
180           115          120          125
181 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
182           130          135          140
183 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val
184           145          150          155          160
185 Tyr Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg
186           165          170          175
187 Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met
188           180          185          190
189 Leu Ala Glu Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu
190           195          200          205
191 Arg Lys Asn Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser
192           210          215          220
193 Glu Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Ser Cys Arg
194           225          230          235          240
195 Glu Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu Leu His Phe Ile
196           245          250          255
197 Met Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys
198           260          265          270
199 Ile Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr
200           275          280          285
201 Glu Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys
202           290          295          300
203 Leu Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu
204           305          310          315          320
205 Lys Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe
206           325          330          335
207 Asn Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile
208           340          345          350
209 Arg Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe
210           355          360          365

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211 Tyr Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu
212      370                      375                      380
213 Leu Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp
214 385                      390                      395                      400
215 Arg Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln
216                      405                      410                      415
217 Lys Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys
218                      420                      425                      430
219 Leu Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala
220                      435                      440                      445
221 Glu Met Leu Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu
222 450                      455                      460
223 Leu Cys Glu Ile Trp Asp Val Gln
224 465                      470
226 <210> SEQ ID NO: 4
227 <211> LENGTH: 462
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapiens
231 <400> SEQUENCE: 4
232 Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
233 1      5      10      15
234 Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser
235      20      25      30
236 Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His
237      35      40      45
238 Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
239 50      55      60
240 Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
241 65      70      75      80
242 Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
243      85      90      95
244 Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
245      100     105     110
246 Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
247      115     120     125
248 Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
249      130     135     140
250 Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
251 145     150     155     160
252 Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
253      165     170     175
254 Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
255      180     185     190
256 Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
257      195     200     205
258 Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
259      210     215     220
260 Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
261 225     230     235     240

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VERIFICATION SUMMARY

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